

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 23:48:08 ; Search time 172 Seconds  
(without alignments)  
74.204 Million cell updates/sec

Title: US-09-674-597A-16  
Perfect score: 165  
Sequence: 1 SVSIOXHXKHLNRSRVERWLKQLQDVHNY 33

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.5	93.6	34	2 AAR07925	Human par
2	154.5	93.6	34	2 AAR07922	Human par
3	154.5	93.6	34	2 AAW20003	Cyclised
4	154.5	93.6	34	2 AAW19997	Cyclised
5	154.5	93.6	34	2 AAW20009	Cyclised
6	154.5	93.6	34	2 AAW17940	Human PTH
7	154.5	93.6	34	2 AAW67275	Parathyro
8	154.5	93.6	34	2 AAW48392	Human par
9	154.5	93.6	34	3 ABJ10720	Human par
10	154.5	93.6	34	3 ABJ10721	Human par
11	154.5	93.6	34	3 ABJ10718	Human par
12	154.5	93.6	34	3 ABJ10747	Human par
13	154.5	93.6	34	3 ABU10750	Human par
14	154.5	93.6	34	3 ABJ10715	Human par
15	154.5	93.6	34	3 ABJ10734	Human par
16	154.5	93.6	34	3 ABJ10745	Human par
17	154.5	93.6	34	3 ABJ10772	Human par
18	154.5	93.6	34	3 ABU10738	Human par
19	154.5	93.6	34	3 ABJ10744	Human par
20	154.5	93.6	34	3 ABJ10709	Human par
21	154.5	93.6	34	3 ABJ10741	Human par
22	154.5	93.6	34	3 ABJ10732	Human par
23	154.5	93.6	34	3 ABU10708	Human par
24	154.5	93.6	34	3 ABJ10711	Human par
25	154.5	93.6	34	3 ABJ10726	Human par

26	154.5	93.6	34	3 ABJ10731	Human par
27	154.5	93.6	34	3 ABU10705	Human par
28	154.5	93.6	34	3 ABJ10725	Human par
29	154.5	93.6	34	3 ABJ10768	Human par
30	154.5	93.6	34	3 ABJ10777	Human par
31	154.5	93.6	34	3 ABJ10728	Human par
32	154.5	93.6	34	3 ABJ10723	Human par
33	154.5	93.6	34	3 ABU10765	Human par
34	154.5	93.6	34	3 ABJ10771	Human par
35	154.5	93.6	34	3 ABJ10773	Human par
36	154.5	93.6	34	3 ABJ10707	Human par
37	154.5	93.6	34	3 ABJ10710	Human par
38	154.5	93.6	34	3 ABJ10716	Human par
39	154.5	93.6	34	3 ABU10762	Human par
40	154.5	93.6	34	3 ABJ10767	Human par
41	154.5	93.6	34	4 AAB96929	Human par
42	154.5	93.6	34	5 AAE18397	Human PTH
43	154.5	93.6	34	5 AAU73033	Parathyro
44	154.5	93.6	34	8 ADF77391	[Nle8,18,
45	154.5	93.6	34	8 ADP18400	Neurogene

## ALIGNMENTS

## RESULT 1

AAR07925  
ID AAR07925 standard; protein; 34 AA.  
XX  
AC AAR07925;  
XX  
DT 18-FEB-1991 (first entry)  
XX  
DE Human parathyroid hormone analogue, Tyr34 Nle8,18 hPTH(7-34).  
XX  
KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 8  
FT /label= Nle  
FT Modified-site 18  
FT /label= Nle  
XX  
PN US4968669-A.  
XX  
PD 06-NOV-1990.  
XX  
PF 21-APR-1989; 89US-00341597.  
XX  
PR 09-MAY-1988; 88US-00191512.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Rosenblatt M, Chorev M;  
XX  
DR WPI; 1990-354642/47.  
XX  
PT New para:thyroid hormone analogues - which inhibit hormone activity by binding receptors while not producing second messenger molecules.  
XX  
PS Claim 1; Col 8; 6pp; English.  
XX  
CC Peptide analogues have high affinity for PTH cell surface receptors, but do not stimulate production of secondary messenger molecules. They may be used in inhibition of PTH action, and in diagnosis and treatment of osteoporosis, hypercalcemia and hyperparathyroidism. Analogues may also be used in treatment of tumours and other cells overproducing peptide hormone-like substances, and immune diseases eg. allergic inflammation and hyperactive lymphocytes. Naturally occurring PTH levels may also be measured in vitro







Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33  
||||| :|||:|||||:|||||:|||||  
Db 1 SVSEIQXHNXGKHLNSXERVEWLRKKLQDVHNY 34

RESULT 8  
AAW48392  
ID AAW48392 standard; peptide; 34 AA.  
AC AAW48392;  
XX  
DT 07-JUL-1998 (first entry)  
XX  
DE Human parathyroid hormone biologically active region.  
XX  
KW Parathyroid hormone related protein; PTH-2 receptor; PTHrP; osteoporosis;  
calcium homeostasis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 5  
FT /note= "Determines signalling capability"  
FT 23  
FT /note= "Determines binding affinity"  
PN WO9804591-A1.  
XX  
PD 05-FEB-1998.  
XX  
PF 30-JUL-1997; 97WO-US013360.  
XX  
PR 31-JUL-1996; 96US-0025471P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (JUEP/) JUEPPNER H.  
XX  
PI Gardella TJ, Jueppner H;  
DR WPI; 1998-130622/12.  
XX  
PT Parathyroid hormone-related peptide analogues with agonist activity - at  
PTHrP/PTHrP receptor and either agonist or antagonist activity at PTH-2  
receptor, used e.g. for treatment of osteoporosis.  
XX  
PS Disclosure; Fig 3; 48pp; English.  
XX  
CC The present sequence represents the biologically active region of human  
parathyroid hormone (PTH). PTH is a major regulator of calcium  
homeostasis whose principal target cells occur in bone and kidney. Some  
of the renal and skeletal actions of PTH appear to be mimicked by PTH  
related protein (PTHrP) which are believed to interact with the PTH  
receptor in these tissues. The invention creates hybrids (AAW48394-  
CC W48398) of the active regions of PTH and PTHrP (AAW48393) to determine  
the residues involved in ligand-specificity of the PTH-2 receptor. It was  
found that ILE 5 determined signalling capabilities while TRP 23  
determined binding affinity. The invention shows that by changing these  
two residues in PTHrP to the corresponding residues in PTH, PTHrP peptide  
analogues are created which are claimed to be selective agonists or  
antagonists of the PTH-2 receptor (AAW48399 and AAW48400). The  
CC antagonistic PTHrP peptide analogues are claimed to be useful in treating  
diseases involving altered or excessive activation of PTH-2 receptors (by  
inhibiting activation) while agonistic PTHrP peptide analogues are  
claimed to be useful in treating osteoporosis (by activating both PTH and  
PTH-2 receptors). PTHrP analogues are also useful for studying biological  
roles of the PTH-2 receptor and to identify specific sites of ligand-  
receptor interaction  
XX  
SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 2; Length 34;

Best Local Similarity 88.2%; Pred. No. 2.5e-12;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNXGKHLNSXERVEWLRKKLQDVHNY 33  
||||| :|||:|||||:|||||:|||||  
Db 1 SVSEIQLMHNLGKHLNSXERVEWLRKKLQDVHNY 34

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ABJ10720  
ID ABJ10720 standard; peptide; 34 AA.  
XX  
AC ABJ10720;  
XX  
DT 02-DEC-2002 (first entry)  
XX  
DE Human parathyroid hormone analogue #16.  
XX  
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
PTHrP; analogue; abnormal CNS function; pancreatic function;  
mineral metabolism; male infertility; abnormal blood pressure;  
hypothalamic disease.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7  
FT /label= OTHER  
FT /note= "OTHER-cyclohexylalanine"  
FT Misc-difference 8  
FT /note= "D-form residue"  
FT Modified-site 11  
FT /label= OTHER  
FT /note= "OTHER-cyclohexylalanine"  
FT Modified-site 18  
FT /label= Nle  
FT Modified-site 34  
FT /note= "C-terminal amide"  
FT Misc-difference 34  
FT /note= "wild-type Phe substituted by Tyr"  
XX  
PN WO9957139-A2.  
XX  
PD 11-NOV-1999.  
XX  
PF 03-MAY-1999; 99WO-US009521.  
XX  
PR 05-MAY-1998; 98US-00072956.  
XX  
PS (SCRC ) SOC CONSEILS RECH & APPL SCI.  
XX  
PI Chorev M, Dong ZX, Rosenblatt M;  
XX  
DR WPI; 2000-038790/03.  
XX  
PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
pancreatic functions, abnormal mineral metabolism and homeostasis, male  
infertility, abnormal blood pressure or hypothalamic disease.  
XX  
PS Claim 11; Page 38; 49pp; English.  
XX  
CC The present invention provides a number of parathyroid hormone (PTH) or  
parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
receptor agonists or antagonists and can be used in the treatment of  
disorders resulting from altered or excessive action of the PTH2  
receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
divergence from normal mineral metabolism and homeostasis, male  
infertility, abnormal blood pressure or a hypothalamic disease. The  
present sequence is a peptide analogue of the invention  
XX  
SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.5e-12;  
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QV 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33  
DB 1 SVSEIQXHNKGKHLNSXERVELRKKLQDVHNY 34

RESULT 10  
ABJ10721  
ID ABJ10721 standard; peptide; 34 AA.

XX AC ABJ10721;  
XX DT 02-DEC-2002 (first entry)

XX DE Human parathyroid hormone analogue #17.

XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
XX KW PTHrP; analogue; abnormal CNS function; pancreatic function;  
XX KW mineral metabolism; male infertility; abnormal blood pressure;  
XX KW hypothalamic disease.

XX OS Homo sapiens.  
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 8 /note= "D-form residue"

FT FT Modified-site 18 /label= Nle

FT FT Modified-site 34 /note= "C-terminal amide"

FT FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"

XX XX WO9957139-A2.

PN PD 11-NOV-1999.

XX PF 03-MAY-1999; 99WO-US009521.

XX PR 05-MAY-1998; 98US-00072956.

XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.

XX PI Chorev M, Dong ZX, Rosenblatt M;

XX DR WPI; 2000-038790/03.

XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
XX PT infertility, abnormal blood pressure or hypothalamic disease.

XX PS Claim 11; Page 38; 49pp; English.

XX CC The present invention provides a number of parathyroid hormone (PTH) or  
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
XX CC receptor agonists or antagonists and can be used in the treatment of  
XX CC disorders resulting from altered or excessive action of the PTH2  
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
XX CC divergence from normal mineral metabolism and homeostasis, male  
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The  
XX CC present sequence is a peptide analogue of the invention

XX SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 91.2%; Pred. No. 2.5e-12;  
Matches 31; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QV 1 SVSEIQ-XHNKGKHLNSXERVELRKKLQDVHNY 33

DB 1 SVSEIQVHNKGKHLNSXERVELRKKLQDVHNY 34

RESULT 11

ABJ10718

ID ABJ10718 standard; peptide; 34 AA.

XX AC ABJ10718;

XX DT 02-DEC-2002 (first entry)

XX DE Human parathyroid hormone analogue #14.

XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
XX KW PTHrP; analogue; abnormal CNS function; pancreatic function;  
XX KW mineral metabolism; male infertility; abnormal blood pressure;  
XX KW hypothalamic disease.

XX OS Homo sapiens.  
XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Modified-site 7 /label= OTHER

FT FT Misc-difference 8 /note= "OTHER=cyclohexylalanine"

FT FT Modified-site 11 /note= "D-form residue"

FT FT Modified-site 18 /label= OTHER

FT FT Modified-site 18 /note= "OTHER=cyclohexylalanine"

FT FT Modified-site 34 /label= Nle

FT FT Misc-difference 34 /note= "C-terminal amide"

FT FT Misc-difference 34 /note= "wild-type Phe substituted by Tyr"

XX XX WO9957139-A2.

PN PD 11-NOV-1999.

XX PF 03-MAY-1999; 99WO-US009521.

XX PR 05-MAY-1998; 98US-00072956.

XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.

XX PI Chorev M, Dong ZX, Rosenblatt M;

XX DR WPI; 2000-038790/03.

XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
XX PT infertility, abnormal blood pressure or hypothalamic disease.

XX PS Claim 11; Page 38; 49pp; English.

XX CC The present invention provides a number of parathyroid hormone (PTH) or  
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
XX CC receptor agonists or antagonists and can be used in the treatment of  
XX CC disorders resulting from altered or excessive action of the PTH2  
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
XX CC divergence from normal mineral metabolism and homeostasis, male  
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The  
XX CC present sequence is a peptide analogue of the invention

XX SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.5e-12;  
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRRKKLQDVHNY 33  
|||||:|||||  
Db 1 SVSEIQXHNKGKHLNSXERVEWLRRKKLQDVHNY 34

RESULT 12  
ABJ10747  
ID ABJ10747 standard; peptide; 34 AA.  
XX  
AC ABJ10747;  
XX  
DT 02-DEC-2002 (first entry)  
XX  
DE Human parathyroid hormone analogue #43.

XX  
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
PTHrP; analogue; abnormal CNS function; pancreatic function;  
KW mineral metabolism; male infertility; abnormal blood pressure;  
KW hypothalamic disease.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
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FT /note= "OTHER=des-Leu"  
FT Modified-site 8  
FT /label= Nle  
FT Modified-site 18  
FT /label= Nle  
FT Modified-site 34  
FT /note= "C-terminal amide"  
FT Misc-difference 34  
FT /note= "wild-type Phe substituted by Tyr"

XX  
PN WO9957139-A2.

XX  
PD 11-NOV-1999.

XX  
PF 03-MAY-1999; 99WO-US009521.

XX  
PR 05-MAY-1998; 98US-00072956.

XX  
PA (SCRC ) SOC CONSEILS RECH & APPL SCI.

XX  
PI Chorev M, Dong ZX, Rosenblatt M;

XX  
DR WPI; 2000-038790/03.

XX  
PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
PT infertility, abnormal blood pressure or hypothalamic disease.

XX  
PS Claim 11; Page 39; 49pp; English.

XX  
CC The present invention provides a number of parathyroid hormone (PTH) or  
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
CC receptor agonists or antagonists and can be used in the treatment of  
CC disorders resulting from altered or excessive action of the PTH2  
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
CC divergence from normal mineral metabolism and homeostasis, male  
CC infertility, abnormal blood pressure or a hypothalamic disease. The  
CC present sequence is a peptide analogue of the invention

XX  
SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.5e-12;  
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRRKKLQDVHNY 33  
|||||:|||||

Db 1 SVSEIQXHNKGKHLNSXERVEWLRRKKLQDVHNY 34

RESULT 13

ABJ10750

ID ABJ10750 standard; peptide; 34 AA.

XX  
AC ABJ10750;

XX  
DT 02-DEC-2002 (first entry)

XX  
DE Human parathyroid hormone analogue #46.

XX  
KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
PTHrP; analogue; abnormal CNS function; pancreatic function;  
KW mineral metabolism; male infertility; abnormal blood pressure;  
KW hypothalamic disease.

XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
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FT /label= Nle  
FT Modified-site 11  
FT /label= OTHER  
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FT /note= "C-terminal amide"  
FT Misc-difference 34  
FT /note= "wild-type Phe substituted by Tyr"

XX  
PN WO9957139-A2.

XX  
PD 11-NOV-1999.

XX  
PF 03-MAY-1999; 99WO-US009521.

XX  
PR 05-MAY-1998; 98US-00072956.

XX  
PA (SCRC ) SOC CONSEILS RECH & APPL SCI.

XX  
PI Chorev M, Dong ZX, Rosenblatt M;

XX  
DR WPI; 2000-038790/03.

XX  
PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
PT infertility, abnormal blood pressure or hypothalamic disease.

XX  
PS Claim 11; Page 39; 49pp; English.

XX  
CC The present invention provides a number of parathyroid hormone (PTH) or  
CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
CC receptor agonists or antagonists and can be used in the treatment of  
CC disorders resulting from altered or excessive action of the PTH2  
CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
CC divergence from normal mineral metabolism and homeostasis, male  
CC infertility, abnormal blood pressure or a hypothalamic disease. The  
CC present sequence is a peptide analogue of the invention

XX  
SQ Sequence 34 AA;

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 97.1%; Pred. No. 2.5e-12;  
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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|||||:|||||

Db 1 SVSEIQXHNKGKHLNSXERVEWLRRKKLQDVHNY 34  
|||||:|||||

RESULT 14  
ABJ10715  
ID ABJ10715 standard; peptide; 34 AA.  
XX AC ABJ10715;  
XX DT 02-DEC-2002 (first entry)  
XX DE Human parathyroid hormone analogue #11.  
XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
KW PTHrP; analogue; abnormal CNS function; pancreatic function;  
KW mineral metabolism; male infertility; abnormal blood pressure;  
XX KW hypothalamic disease.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 7 /label= OTHER  
FT /note= "OTHER=cyclohexylalanine"  
FT Misc-difference 8  
FT /note= "D-form residue"  
FT Modified-site 11  
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FT /note= "OTHER=cyclohexylalanine"  
FT Modified-site 18  
FT /label= Nle  
FT Modified-site 34  
FT /note= "C-terminal amide"  
FT Misc-difference 34  
FT /note= "wild-type Phe substituted by Tyr"  
XX PN WO9957139-A2.  
XX PD 11-NOV-1999.  
XX PP 03-MAY-1999; 99WO-US009521.  
XX PR 05-MAY-1998; 98US-00072956.  
XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.  
XX PI Chorev M, Dong ZX, Rosenblatt M;  
XX DR WPI; 2000-038790/03.  
XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
XX PT infertility, abnormal blood pressure or hypothalamic disease.  
XX PS Claim 11; Page 38; 49pp; English.  
XX CC The present invention provides a number of parathyroid hormone (PTH) or  
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
XX CC receptor agonists or antagonists and can be used in the treatment of  
XX CC disorders resulting from altered or excessive action of the PTH2  
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
XX CC divergence from normal mineral metabolism and homeostasis, male  
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The  
XX CC present sequence is a peptide analogue of the invention  
XX SQ Sequence 34 AA;  
Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.5e-12;  
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
Oy 1 SVSEIQ-XHNKXGHLNKSXERVEWLRLKQLDVHNY 33  
Db 1 SVSEIQXHNKXGHLNKSXERVEWLRLKQLDVHNY 34

RESULT-15  
ABJ10734  
ID ABJ10734 standard; peptide; 34 AA.  
XX AC ABJ10734;  
XX DT 02-DEC-2002 (first entry)  
XX DE Human parathyroid hormone analogue #30.  
XX KW Human; parathyroid hormone; parathyroid hormone-related protein; PTH;  
KW PTHrP; analogue; abnormal CNS function; pancreatic function;  
KW mineral metabolism; male infertility; abnormal blood pressure;  
XX KW hypothalamic disease.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
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FT /note= "OTHER=cyclohexylalanine"  
FT Misc-difference 8  
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FT /note= "C-terminal amide"  
FT Misc-difference 34  
FT /note= "wild-type Phe substituted by Tyr"  
XX PN WO9957139-A2.  
XX PD 11-NOV-1999.  
XX PP 03-MAY-1999; 99WO-US009521.  
XX PR 05-MAY-1998; 98US-00072956.  
XX PA (SCRC ) SOC CONSEILS RECH & APPL SCI.  
XX PI Chorev M, Dong ZX, Rosenblatt M;  
XX DR WPI; 2000-038790/03.  
XX PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or  
XX PT pancreatic functions, abnormal mineral metabolism and homeostasis, male  
XX PT infertility, abnormal blood pressure or hypothalamic disease.  
XX PS Claim 11; Page 38; 49pp; English.  
XX CC The present invention provides a number of parathyroid hormone (PTH) or  
XX CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2  
XX CC receptor agonists or antagonists and can be used in the treatment of  
XX CC disorders resulting from altered or excessive action of the PTH2  
XX CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,  
XX CC divergence from normal mineral metabolism and homeostasis, male  
XX CC infertility, abnormal blood pressure or a hypothalamic disease. The  
XX CC present sequence is a peptide analogue of the invention  
XX SQ Sequence 34 AA;  
Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 97.1%; Pred. No. 2.5e-12;  
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Oy 1 SVSEIQ-XHNKXGHLNKSXERVEWLRLKQLDVHNY 33



Db 1 SVSEIQXXHXXGKHLNSXERVELRKKQDVHNY 34

Search completed: April 2, 2005, 00:08:39  
Job time : 175 secs

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OM protein - protein search, using sw model

Run on: April 2, 2005, 00:05:01 ; Search time 42 Seconds  
(without alignments)  
58.653 Million cell updates/sec

Title: US-09-674-597A-16  
Perfect score: 165  
Sequence: 1 SVSEIQXNKGKHLNRSRVERWLRKQLQDVNY 33

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
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5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.5	93.6	34	1 US-08-488-105-10	Sequence 10, Appl
2	154.5	93.6	34	2 US-08-142-551B-3	Sequence 3, Appl
3	154.5	93.6	34	3 US-08-903-497A-1	Sequence 1, Appl
4	154.5	93.6	34	4 US-09-635-076-1	Sequence 1, Appl
5	154.5	93.6	34	5 US-09-843-221A-21	Sequence 21, Appl
6	154.5	93.6	35	6 US-08-142-551B-4	Sequence 4, Appl
7	154.5	93.6	35	7 US-08-142-551B-5	Sequence 5, Appl
8	154.5	93.6	35	8 US-08-142-551B-7	Sequence 7, Appl
9	154.5	93.6	35	9 US-08-142-551B-23	Sequence 23, Appl
10	154.5	93.6	35	10 US-08-142-551B-31	Sequence 31, Appl
11	154.5	93.6	35	11 US-08-142-551B-32	Sequence 32, Appl
12	154.5	93.6	35	12 US-08-142-551B-33	Sequence 33, Appl
13	154.5	93.6	35	13 US-08-142-551B-34	Sequence 34, Appl
14	154.5	93.6	35	14 US-08-142-551B-35	Sequence 35, Appl
15	154.5	93.6	35	15 US-08-142-551B-36	Sequence 36, Appl
16	154.5	93.6	35	16 US-08-142-551B-37	Sequence 37, Appl
17	154.5	93.6	35	17 US-08-142-551B-44	Sequence 44, Appl
18	154.5	93.6	35	18 US-08-142-551B-45	Sequence 45, Appl
19	154.5	93.6	35	19 US-08-142-551B-46	Sequence 46, Appl
20	154.5	93.6	35	20 US-08-142-551B-49	Sequence 49, Appl
21	154.5	93.6	35	21 US-08-142-551B-67	Sequence 67, Appl
22	154.5	93.6	35	22 US-08-142-551B-68	Sequence 68, Appl
23	154.5	93.6	35	23 US-08-142-551B-70	Sequence 70, Appl
24	154.5	93.6	35	24 US-08-142-551B-73	Sequence 73, Appl
25	154.5	93.6	35	25 US-08-142-551B-80	Sequence 80, Appl
26	154.5	93.6	35	26 US-08-142-551B-90	Sequence 90, Appl
27	154.5	93.6	35	27 US-08-142-551B-94	Sequence 94, Appl

28 154.5 93.6 44 1 US-08-468-275-4 Sequence 4, Appl  
29 154.5 93.6 44 3 US-09-007-466-4 Sequence 4, Appl  
30 154.5 93.6 44 3 US-08-952-980B-4 Sequence 4, Appl  
31 154.5 93.6 67 2 US-08-142-551B-9 Sequence 9, Appl  
32 151.5 91.8 35 2 US-08-142-551B-30 Sequence 30, Appl  
33 151.5 91.8 35 2 US-08-142-551B-50 Sequence 50, Appl  
34 151.5 91.8 35 2 US-08-142-551B-72 Sequence 72, Appl  
35 151.5 91.8 35 2 US-08-142-551B-88 Sequence 88, Appl  
36 151.5 91.8 35 2 US-08-142-551B-91 Sequence 91, Appl  
37 151.5 91.8 35 2 US-08-142-551B-95 Sequence 95, Appl  
38 151.5 91.8 35 2 US-07-765-373-1 Sequence 102, Appl  
39 150.5 91.2 34 1 US-08-033-099-1 Sequence 1, Appl  
40 150.5 91.2 34 1 US-08-262-495C-1 Sequence 1, Appl  
41 150.5 91.2 34 1 US-07-915-247A-1 Sequence 1, Appl  
42 150.5 91.2 34 1 US-08-443-863-1 Sequence 1, Appl  
43 150.5 91.2 34 1 US-08-448-070-1 Sequence 1, Appl  
44 150.5 91.2 34 1 US-08-488-105-4 Sequence 4, Appl  
45 150.5 91.2 34 1 US-08-488-105-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-488-105-10  
; Sequence 10, Application US/08488105  
; Patent No. 5717062  
; GENERAL INFORMATION:  
; APPLICANT: Chorev, Michael  
; APPLICANT: Rosenblatt, Michael  
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,105  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsao, Y. Rocky  
; REGISTRATION NUMBER: 34,053  
; REFERENCE/DOCKET NUMBER: 00537/112001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; OTHER INFORMATION: The side chains of Lys at  
; position 26 and Asp at position 30 are linked by an amide bond  
; and this sequence has an amide C-terminus (i.e., CONH2), rather  
; than a carboxy C-terminus (i.e., COOH).  
; FEATURE:  
; OTHER INFORMATION: Xaa at positions 8 and 18  
; OTHER INFORMATION: are No. 5717062leucine.  
US-08-488-105-10

Query Match 93.6%; Score 154.5; DB 1; Length 34;  
Best Local Similarity 94.1%; Pred. No. 6.8e-13;  
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRKKLQDVHNY 33  
Db 1 SVSEIQLHNLGKHLNSKXRVWLRKKLQDVHNY 34

RESULT 2  
US-08-142-551B-3  
; Sequence 3, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/898,219  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-142-551B-3

Query Match 93.6%; Score 154.5; DB 2; Length 34;  
Best Local Similarity 88.2%; Pred. No. 6.8e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRKKLQDVHNY 33  
Db 1 SVSEIQLHNLGKHLNSKXRVWLRKKLQDVHNY 34

RESULT 3  
US-08-903-497A-1  
; Sequence 1, Application US/08903497A  
; Patent No. 6147186  
; GENERAL INFORMATION:

; APPLICANT: Gardella, Thomas J.  
; APPLICANT: J pper, Harald  
; TITLE OF INVENTION: No. 6147186el Parathyroid Hormone-Related  
; TITLE OF INVENTION: Peptide Analogs  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/903,497A  
; FILING DATE: 30-JUL-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/025,471  
; FILING DATE: 31-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Markowicz, Karen R.  
; REGISTRATION NUMBER: 36,351  
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: MODIFIED-SITE  
; LOCATION: 34  
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-AMIDE  
US-08-903-497A-1

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 88.2%; Pred. No. 6.8e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSKXRVWLRKKLQDVHNY 33  
Db 1 SVSEIQLHNLGKHLNSKXRVWLRKKLQDVHNY 34

RESULT 4  
US-09-635-076-1  
; Sequence 1, Application US/09635076  
; Patent No. 6362163  
; GENERAL INFORMATION:  
; APPLICANT: Gardella, Thomas J.  
; APPLICANT: J pper, Harald  
; TITLE OF INVENTION: No. 6362163el Parathyroid Hormone-Related  
; TITLE OF INVENTION: Peptide Analogs  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/635,076  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/903,497  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Markowicz, Karen R.  
REGISTRATION NUMBER: 36,351  
REFERENCE/DOCKET NUMBER: 0609,4310001/JAG/KRM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: MODIFIED-SITE  
LOCATION: 34  
OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-  
OTHER INFORMATION: AMIDE  
US-09-635-076-1

Query Match 93.6%; Score 154.5; DB 3; Length 34;  
Best Local Similarity 88.2%; Pred. No. 6.8e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33  
DB 1 SVSEIQLHNLGKHLNSERVEWLRKKLQDVHNY 34

## RESULT 5

US-09-843-221A-21  
Sequence 21, Application US/09843221A  
Patent No. 6756480  
GENERAL INFORMATION:  
APPLICANT: KOSTENUK, PAUL  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: LACEY, DAVID LEE  
TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
TITLE OF INVENTION: RELATED PROTEIN  
FILE REFERENCE: A-665B  
CURRENT APPLICATION NUMBER: US/09/843,221A  
CURRENT FILING DATE: 2001-04-26  
PRIOR APPLICATION NUMBER: 60/266,673  
PRIOR FILING DATE: 2001-02-06  
PRIOR APPLICATION NUMBER: 60/214,860  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 60/200,053  
PRIOR FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 21  
LENGTH: 34  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified human PTH  
US-09-843-221A-21

Query Match 93.6%; Score 154.5; DB 4; Length 34;  
Best Local Similarity 88.2%; Pred. No. 6.8e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33  
DB 1 SVSEIQLHNLGKHLNSERVEWLRKKLQDVHNY 34  
RESULT 6  
US-08-142-551B-4  
Sequence 4, Application US/08142551B  
Patent No. 5814603  
GENERAL INFORMATION:  
APPLICANT: Oldenburg, Kevin R.  
APPLICANT: Selick, Harold E.  
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
NUMBER OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: US  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,551B  
FILING DATE: 25-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,296  
FILING DATE: 14-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,219  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,677  
FILING DATE: 22-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swisse, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 854-7400  
TELEFAX: (415) 854-8275  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 35  
OTHER INFORMATION: /note= "Where "Xaa" is Homoserine  
OTHER INFORMATION: Lactone"  
US-08-142-551B-4

Query Match 93.6%; Score 154.5; DB 2; Length 35;  
Best Local Similarity 88.2%; Pred. No. 7.1e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33  
DB 1 SVSEIQLHNLGKHLNSERVEWLRKKLQDVHNY 34

## RESULT 7

US-08-142-551B-5  
Sequence 5, Application US/08142551B  
Patent No. 5814603

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; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-142-551B-7

Query Match          93.6%; Score 154.5; DB 2; Length 33
Best Local Similarity 88.2%; Pred. No. 7.le-13;
Matches 30; Conservative 3; Mismatches 0; Indels

QY      1 SVSETQ-XHNKGKHLNSXRVWLRKKLQDVHNY 33
       |||||:|:::|||||:|||||:|||||
DB      1 SVSETQLLNGLKHLNLSRVLWRKKLQDVHNY 34

RESULT 9
US-08-142-551B-23
; Sequence 23, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296

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; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
US-08-142-551B-23
Query Match 93.6%; Score 154.5; DB 2; Length 35;
Best Local Similarity 88.2%; Pred. No. 7,1e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLRKKLQDVHNY 33
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Db 1 SVSEIQHLNLGKHLNSLVRVWLRKKLQDVHNY 34

RESULT 10
US-08-142-551B-31
; Sequence 31, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
;
US-08-142-551B-31
Query Match 93.6%; Score 154.5; DB 2; Length 35;
Best Local Similarity 88.2%; Pred. No. 7,1e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLRKKLQDVHNY 33
      ||||| :||:|||||:|||||:|||||
Db 1 SVSEIQHLNLGKHLNSLVRVWLRKKLQDVHNY 34

RESULT 11
US-08-142-551B-32
; Sequence 32, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
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; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-32
Query Match 93.6%; Score 154.5; DB 2; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.1e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQRLNKLKHLNSLRLVWLKRLQDVHNY 34

RESULT 12
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; Sequence 33, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142.551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-33
Query Match 93.6%; Score 154.5; DB 2; Length 35;
Best Local Similarity 88.2%; Pred. No. 7.1e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLKRLQDVHNY 33
Db 1 SVSEIQRLNKLKHLNSLRLVWLKRLQDVHNY 34

RESULT 13
US-08-142-551B-34
; Sequence 34, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142.551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 35
; OTHER INFORMATION: /note= "Xaa" is selected
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine
; OTHER INFORMATION: amide, or the sequence of amino acids comprising
; OTHER INFORMATION: residues 35-84 of PTH."
; US-08-142-551B-34

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Query Match 93.6%; Score 154.5; DB 2; Length 35;  
Best Local Similarity 88.2%; Pred. No. 7.1e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNLSRVERWLKRLKLDVHNY 33  
DB 1 SVSEIQGLNGLKHLNLSRVERWLKRLKLDVHNY 34

RESULT 14  
US-08-142-551B-35  
; Sequence 35, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 35  
; OTHER INFORMATION: /note= "Where "Xaa" is selected  
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine  
; OTHER INFORMATION: amide, or the sequence of amino acids comprising  
; OTHER INFORMATION: residues 35-84 of PTH."

US-08-142-551B-35

Query Match 93.6%; Score 154.5; DB 2; Length 35;  
Best Local Similarity 88.2%; Pred. No. 7.1e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;  
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DB 1 SVSEIQGLNGLKHLNLSRVERWLKRLKLDVHNY 34

Query Match 93.6%; Score 154.5; DB 2; Length 35;  
Best Local Similarity 88.2%; Pred. No. 7.1e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNLSRVERWLKRLKLDVHNY 33  
DB 1 SVSEIQGLNGLKHLNLSRVERWLKRLKLDVHNY 34

DB 1 SVSEIQGLNGLKHLNLSRVERWLKRLKLDVHNY 34

RESULT 15  
US-08-142-551B-36  
; Sequence 36, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND  
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME  
; NUMBER OF SEQUENCES: 132  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: US  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,551B  
; FILING DATE: 25-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/077,296  
; FILING DATE: 14-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,677  
; FILING DATE: 22-OCT-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-7400  
; TELEFAX: (415) 854-8275  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 35  
; OTHER INFORMATION: /note= "Where "Xaa" is selected  
; OTHER INFORMATION: from the group consisting of Hol, Ho, a homoserine  
; OTHER INFORMATION: amide, or the sequence of amino acids comprising  
; OTHER INFORMATION: residues 35-84 of PTH."

US-08-142-551B-36

Query Match 93.6%; Score 154.5; DB 2; Length 35;  
Best Local Similarity 88.2%; Pred. No. 7.1e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNLSRVERWLKRLKLDVHNY 33  
DB 1 SVSEIQGLNGLKHLNLSRVERWLKRLKLDVHNY 34

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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Title: US-09-674-597A-16  
Perfect score: 165  
Sequence: 1 SVSEIQXHNKXGHLNLSRVERWLRKQLQDVHNY 33

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Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

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- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154.5	93.6	34	10	US-09-843-221A-21
2	154.5	93.6	34	15	US-10-311-366-15
3	154.5	93.6	34	17	US-10-718-071-14
4	150.5	91.2	34	9	US-09-169-786-3
5	150.5	91.2	34	9	US-09-858-880-5
6	150.5	91.2	34	9	US-09-928-047B-6
7	150.5	91.2	34	10	US-09-843-221A-16
8	150.5	91.2	34	10	US-09-843-221A-17
9	150.5	91.2	34	10	US-09-843-221A-18
10	150.5	91.2	34	10	US-09-843-221A-161
11	150.5	91.2	34	10	US-09-843-221A-162
12	150.5	91.2	34	10	US-09-843-221A-163
13	150.5	91.2	34	10	US-09-928-048A-6

14	150.5	91.2	34	13	US-10-016-403-5	Sequence 5, Appli
15	150.5	91.2	34	13	US-10-097-079-1	Sequence 1, Appli
16	150.5	91.2	34	14	US-10-361-928-8	Sequence 8, Appli
17	150.5	91.2	34	14	US-10-340-484-15	Sequence 15, Appl
18	150.5	91.2	34	14	US-10-340-484-16	Sequence 16, Appl
19	150.5	91.2	34	14	US-10-340-484-17	Sequence 17, Appl
20	150.5	91.2	34	15	US-10-427-259-2	Sequence 2, Appli
21	150.5	91.2	34	15	US-10-398-449-14	Sequence 14, Appl
22	150.5	91.2	34	15	US-10-398-449-18	Sequence 18, Appl
23	150.5	91.2	34	15	US-10-311-366-13	Sequence 13, Appl
24	150.5	91.2	34	15	US-10-440-473-1	Sequence 1, Appli
25	150.5	91.2	34	15	US-10-443-693-2	Sequence 2, Appli
26	150.5	91.2	34	17	US-10-484-080-31	Sequence 31, Appl
27	150.5	91.2	34	17	US-10-638-265-82	Sequence 82, Appl
28	150.5	91.2	34	17	US-10-892-025-4	Sequence 4, Appli
29	150.5	91.2	35	17	US-10-892-025-5	Sequence 5, Appli
30	150.5	91.2	36	17	US-10-892-025-6	Sequence 6, Appli
31	150.5	91.2	37	14	US-10-168-185-9	Sequence 9, Appli
32	150.5	91.2	37	16	US-10-466-483A-8	Sequence 8, Appli
33	150.5	91.2	37	17	US-10-892-025-7	Sequence 7, Appli
34	150.5	91.2	38	9	US-09-169-786-4	Sequence 4, Appli
35	150.5	91.2	38	10	US-09-843-221A-14	Sequence 14, Appl
36	150.5	91.2	38	14	US-10-245-707-1	Sequence 1, Appli
37	150.5	91.2	38	15	US-10-398-449-20	Sequence 20, Appl
38	150.5	91.2	38	15	US-10-311-366-18	Sequence 18, Appl
39	150.5	91.2	38	17	US-10-892-025-8	Sequence 8, Appli
40	150.5	91.2	39	17	US-10-892-025-9	Sequence 9, Appli
41	150.5	91.2	40	17	US-10-892-025-10	Sequence 10, Appl
42	150.5	91.2	41	17	US-10-892-025-11	Sequence 11, Appl
43	150.5	91.2	42	13	US-10-024-918-28	Sequence 28, Appl
44	150.5	91.2	42	14	US-10-323-021-17	Sequence 17, Appl
45	150.5	91.2	42	14	US-10-323-046-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1  
US-09-843-221A-21  
; Sequence 21, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENIUK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HC  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified human PTH  
US-09-843-221A-21

Query Match 93.6%; Score 154.5; DB 10; Length 34;  
Best Local Similarity 88.2%; Pred. No. 6.8e-12;  
Matches 30; Conservative 3; Mismatches 0; Indels 1; Gaps 1;  
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DB 1 SVSEIQLLNKXGHLNLSRVERWLRKQLQDVHNY 34

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RESULT 2
US-10-311-366-15
; Sequence 15, Application US/10311366
; Publication No. US20040022838A1
; GENERAL INFORMATION:
; APPLICANT: Hollick, Michael F.
; TITLE OF INVENTION: Regulation Of Cell Proliferation And Differentiation Using Topical
; TITLE OF INVENTION: Applied Peptides
; FILE REFERENCE: 1539.0310001
; CURRENT APPLICATION NUMBER: US/10/311.366
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19650
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/213,247
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (18)..(18)
; OTHER INFORMATION: Nle
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: [Nle8,18, Tyr34] hPTH (1-34)
US-10-311-366-15
Query Match 93.6%; Score 154.5; DB 15; Length 34;
Best Local Similarity 94.1%; Pred. No. 6.8e-12;
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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Db 1 SVSEIQLXHNGLGKHLNSXERVEWLRKKLQDVHNY 34
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RESULT 3
US-10-718-071-14
; Sequence 14, Application US/10718071
; Publication No. US20050009847A1
; GENERAL INFORMATION:
; APPLICANT: Bertilsson, Goran
; APPLICANT: Eriandson, Rikard
; APPLICANT: Frisen, Jonas
; APPLICANT: Haegerstrand, Anders
; APPLICANT: Heidrich, Jessica
; APPLICANT: Hellstrom, Kristina
; APPLICANT: Hagblad, Johan
; APPLICANT: Jamson, Katarina
; APPLICANT: Kortsemaa, Jarkko
; APPLICANT: Lindquist, Per
; APPLICANT: Lundh, Hanna
; APPLICANT: McGuire, Jacqueline
; APPLICANT: Mercer, Alex
; APPLICANT: Nyberg, Karl
; APPLICANT: Ossolinak, Amina
; APPLICANT: Patrone, Cesare
; APPLICANT: Ronnholm, Harriet
; APPLICANT: Wirkstrom, Lilian
; APPLICANT: Zachrisson, Olof
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
; FILE REFERENCE: 21882-517 UTIL
; CURRENT APPLICATION NUMBER: US/10/718.071
; CURRENT FILING DATE: 2003-11-20

US-09-674-597a-16.dx.rapb
; PRIOR APPLICATION NUMBER: US 60/427,912
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: norleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: norleucine
US-10-718-071-14
Query Match 93.6%; Score 154.5; DB 17; Length 34;
Best Local Similarity 94.1%; Pred. No. 6.8e-12;
Matches 32; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| |||:|||||:|||||:|||||:|||||
Db 1 SVSEIQLXHNGLGKHLNSXERVEWLRKKLQDVHNY 34
||||| |||:|||||:|||||:|||||:|||||

RESULT 4
US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169.786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3
Query Match 91.2%; Score 150.5; DB 9; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
||||| |||:|||||:|||||:|||||:|||||
Db 1 SVSEIQLXHNGLGKHLNSXERVEWLRKKLQDVHNF 34
||||| |||:|||||:|||||:|||||:|||||

RESULT 5
US-09-858-880-5
; Sequence 5, Application US/09858880
; Publication No. US20020061838A1
; GENERAL INFORMATION:
; APPLICANT: Holmquist, Barton
; APPLICANT: Dormady, Daniel
; TITLE OF INVENTION: Peptide Pharmaceutical Formulations
; FILE REFERENCE: 1627.020US1
; CURRENT APPLICATION NUMBER: US/09/858.880
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,377
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/205,262
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-880-5

Query Match          91.2%; Score 150.5; DB 9; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
    ||||| :||:|||||:|||||:|||||:
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6
US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match          91.2%; Score 150.5; DB 9; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
    ||||| :||:|||||:|||||:|||||:
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7
US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match          91.2%; Score 150.5; DB 10; Length 34;
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```
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
    ||||| :||:|||||:|||||:|||||:
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8
US-09-843-221A-17
; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17

Query Match          91.2%; Score 150.5; DB 10; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVEWLRKKLQDVHNY 33
    ||||| :||:|||||:|||||:|||||:
Db 1 SVSEIQLMHNLRGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9
US-09-843-221A-18
; Sequence 18, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-18
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## US-09-843-221A-18

Query Match 91.2%; Score 150.5; DB 10; Length 34;  
Best Local Similarity 85.3%; Pred. No. 2.1e-11;  
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 SVSEIQLMHNKGLNSRVERWLKRLKLDVHNF 34

## RESULT 10

US-09-843-221A-161  
; Sequence 161, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 161  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus  
US-09-843-221A-161

Query Match 91.2%; Score 150.5; DB 10; Length 34;  
Best Local Similarity 85.3%; Pred. No. 2.1e-11;  
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 SVSEIQLMHNKGLNSRVERWLKRLKLDVHNF 34

## RESULT 11

US-09-843-221A-162  
; Sequence 162, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 162  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - PTH  
; NAME/KEY: misc feature  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus  
US-09-843-221A-162

Query Match 91.2%; Score 150.5; DB 10; Length 34;  
Best Local Similarity 85.3%; Pred. No. 2.1e-11;  
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 SVSEIQLMHNKGLNSRVERWLKRLKLDVHNF 34

## RESULT 12

US-09-843-221A-163  
; Sequence 163, Application US/09843221A  
; Publication No. US20030039654A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENUIK, PAUL  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: LACEY, DAVID LEE  
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H  
; TITLE OF INVENTION: RELATED PROTEIN  
; FILE REFERENCE: A-665B  
; CURRENT APPLICATION NUMBER: US/09/843,221A  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: 60/266,673  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/214,860  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/200,053  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 163  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Preferred embodiments - PTH  
; NAME/KEY: misc feature  
; LOCATION: (34)..(34)  
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus  
US-09-843-221A-163

Query Match 91.2%; Score 150.5; DB 10; Length 34;  
Best Local Similarity 85.3%; Pred. No. 2.1e-11;  
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNXGKHLNSXRVWLKRLKLDVHNY 33  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1 SVSEIQLMHNKGLNSRVERWLKRLKLDVHNF 34

## RESULT 13

US-09-928-048A-6  
; Sequence 6, Application US/09928048A  
; Publication No. US20030138858A1  
; GENERAL INFORMATION:  
; APPLICANT: Scantibodies Laboratory, Inc.  
; APPLICANT: Cantor, Thomas L.  
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT  
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE  
; FILE REFERENCE: 53221-20015.00  
; CURRENT APPLICATION NUMBER: US/09/928,048A  
; CURRENT FILING DATE: 2000-08-10

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match      91.2%; Score 150.5; DB 10; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
    ||||| :||:||||:||||:||||:||||:
Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

RESULT 14
US-10-016-403-5
; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; CORRESPONDENCE ADDRESS: INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match      91.2%; Score 150.5; DB 13; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
    ||||| :||:||||:||||:||||:||||:
Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34
```

```

RESULT 15
US-10-097-079-1
; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: No. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

Query Match      91.2%; Score 150.5; DB 13; Length 34;
Best Local Similarity 85.3%; Pred. No. 2.1e-11;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXERVWLRKKLQDVHNY 33
    ||||| :||:||||:||||:||||:||||:
Db 1 SVSEIQLMHNLGKHLNSMERVWLRKKLQDVHNF 34

Search completed: April 2, 2005, 00:15:50
Job time : 142 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 23:53:04 ; Search time 43 Seconds  
(without alignments)  
73.841 Million cell updates/sec

Title: US-09-674-597A-16  
Perfect score: 165  
Sequence: j SVSEIQHXNKGHLNXXRVEWLKQLQDVHNY 33  
Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150.5	91.2	115	1 PTHG	parathyroid hormon
2	145.5	88.2	115	1 PTHG	parathyroid hormon
3	145.5	88.2	115	2 JCA202	parathyroid hormon
4	142.5	86.4	115	1 PTBO	parathyroid hormon
5	133.5	80.9	115	2 A05091	parathyroid hormon
6	125.5	76.1	105	2 I51851	parathyroid hormon
7	102.5	62.1	119	2 A34937	parathyroid hormon
8	65	39.4	3678	2 S28916	dyatrophin - mouse
9	62	37.6	1257	1 I58383	retinoblastoma bin
10	60	36.4	764	1 BBHU	complement factor
11	58.5	35.5	1172	2 T00065	hypothetical prote
12	58	35.2	3685	1 A27605	dystrophin, muscle
13	57	34.5	118	2 T44470	transposase tnpD I
14	57	34.5	240	1 TQSC34	transposase - Esch
15	57	34.5	296	2 S0261	probable transposa
16	56	33.9	334	2 F84662	AlGI-like protein,
17	56	33.9	898	2 C84854	hypothetical prote
18	55	33.3	513	1 R98CAY	transcription regu
19	55	33.3	513	2 F90866	transcription regu
20	55	33.3	513	2 C85752	hypothetical prote
21	54	32.7	229	2 E85806	hypothetical prote
22	54	32.7	229	2 D90958	hypothetical prote
23	54	32.7	286	2 B69834	conserved hypothet
24	54	32.7	295	2 F90938	hypothetical prote
25	54	32.7	295	2 B85664	transposase for IS
26	54	32.7	295	2 D90801	hypothetical prote
27	54	32.7	295	2 B85613	probable transposa
28	54	32.7	295	2 B85787	probable transposa
29	54	32.7	295	2 T00315	transposase - Esch

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: proparathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence revision 19-Jan-1996 #text change 09-Jul-2004

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410; 138;

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr., J.T.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: UNIPROT:P01270; GB:J00301; NID:gl90702; PIDN:AAA60215.1; PID:gl90704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid hormone des

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X',33,'X',35-46;65-84;105-110 <YAM>

A>Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occurred

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human parathyroid hormone by a new microsequencing ap

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olatad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingamo, O.R.; Gautvik, V.T.

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated forms c

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114,'N' <OLS>

A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylation;

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L.H.;

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyroid t

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residues 1-

A:Reference number: A93783; MUID:73070429; PMID:4509319

A:Accession: A93783

A:Molecule type: protein



Db 32 SVSEIQFMNHLGKHLSSMERVEWLKRLKQDVHNF 65

## RESULT 4

PTBO

parathyroid hormone precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
C:Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534  
R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.  
Gene 28, 319-329, 1984  
A>Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroid hormone  
A:Reference number: A24949; MUID:84262483; PMID:6086460  
A:Accession: A24949  
A:Molecule type: DNA  
A:Residues: 1-115 <WEA>  
A:Cross-references: UNIPROT:P01268; GB:K01938  
R:Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr., R.  
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979  
A>Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone  
A:Reference number: A93835; MUID:80056617; PMID:388425  
A:Accession: A93835  
A:Molecule type: DNA  
A:Residues: 1-115 <KRO>  
A:Cross-references: GB:J00023; NID:984; PIDN:CAA23439.1; PID:985  
A>Note: the authors translated the codon GAA for residue 50 as Gly  
R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn, D.V.  
Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974  
A>Title: The N-terminal amino-acid sequence of bovine parathyroid hormone.  
A:Reference number: A93793; MUID:74142666; PMID:4522780  
A:Accession: A93793  
A:Molecule type: protein  
A:Residues: 26-115 <HAM>  
R:Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Potts Jr., R.; Hoppe-Seyler, Z.  
Physiol. Chem. 351, 1586-1588, 1970  
A>Title: The amino acid sequence of bovine parathyroid hormone I.  
A:Reference number: A91648; MUID:71076162; PMID:5531031  
A:Accession: A91648  
A:Molecule type: protein  
A:Residues: 32-115 <NTA>  
R:Brewer Jr., H.B.; Ronan, R.  
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970  
A>Title: Bovine parathyroid hormone: amino acid sequence.  
A:Reference number: A93773; MUID:71063634; PMID:5275384  
A:Accession: A93773  
A:Molecule type: protein  
A:Residues: 32-115 <BRE>  
R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.; Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971  
A>Title: Synthesis of a biologically active N-terminal tetrapeptide of parathyroid hormone  
A:Reference number: A93776; MUID:71091588; PMID:4322265  
A:Contents: annotation; synthesis of residues 32-65  
A>Note: the synthetic peptide was active in vivo and in vitro  
R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littlelike, T.; Arnaud, C.D.  
Am. J. Med. 56, 759-766, 1974  
A>Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone  
A:Reference number: A90030; MUID:74173303; PMID:4598526  
A:Contents: annotation  
R:Weaver, C.A.; Gordon, D.F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981  
A>Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene  
A:Reference number: I45975; MUID:82037785; PMID:6170060  
A:Accession: I45975  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <WE2>  
A:Cross-references: GB:J00024; NID:9163642; PIDN:AAA30747.1; PID:9163643  
R:Weaver, C.A.; Gordon, D.F.  
Mol. Cell. Endocrinol. 28, 411-424, 1982  
A>Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.  
A:Reference number: I45976; MUID:83105964; PMID:6185374  
A:Accession: I45976  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-115 <WE3>  
A:Cross-references: GB:M25082; NID:9163644; PIDN:AAA30748.1; PID:9163645  
C:Genetics: PTH  
A:Gene: PTH  
A:Introns: 29/2  
C:Superfamily: parathyroid hormone; parathyroid hormone homology  
C:Keywords: hormone  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-115/Product: parathyroid hormone #status experimental <PMAT>  
F:26-31/Domain: propeptide #status experimental <PRO>  
F:30-64/Domain: parathyroid hormone homology <PTH>  
F:32-115/Product: parathyroid hormone #status experimental <MAT>

Query Match 86.4%; Score 142.5; DB 1; Length 115;  
Best Local Similarity 79.4%; Pred. No. 4.2e-10;  
Matches 27; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

QY 1 SVSEIQ-FHNKXGKHLSSMERVEWLKRLKQDVHNY 33  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 32 AVSEIQFMNHLGKHLSSMERVEWLKRLKQDVHNF 65

## RESULT 5

A05091

parathyroid hormone precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004

C:Accession: A05091; A26806

R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.

J. Biol. Chem. 259, 3320-3329, 1984

A:Reference number: A05091; MUID:84135846; PMID:6321505

A:Accession: A05091

A:Molecule type: DNA

A:Residues: 1-115 &lt;HEI&gt;

A:Cross-references: UNIPROT:P04089; GB:K01268; NID:9206483; PIDN:AAA1979.1; PID:9206485

A&gt;Note: the authors translated the codon GAA for residue 87 as Asp

R:Schmelzer, H.J.; Gross, G.; Wiedera, G.; Mayer, H.

Nucleic Acids Res. 15, 6740, 1987

A&gt;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone

A:Reference number: A26806; MUID:87316938; PMID:3628009

A:Accession: A26806

A&gt;Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-115 &lt;SCH&gt;

A:Cross-references: GB:X05721; GB:Y00409; NID:956002; PIDN:CAA29192.1; PID:956003

C:Genetics:

A:Introns: 29/3

C:Superfamily: parathyroid hormone; parathyroid hormone homology

F:30-64/Domain: parathyroid hormone homology &lt;PTH&gt;

Query Match 80.9%; Score 133.5; DB 2; Length 115;  
Best Local Similarity 73.5%; Pred. No. 5.1e-09;  
Matches 25; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVSEIQ-FHNKXGKHLSSMERVEWLKRLKQDVHNY 33  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 32 AVSEIQFMNHLGKHLSSMERVEWLKRLKQDVHNF 65

## RESULT 6

I51851

parathyroid hormone - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999

C:Accession: I51851

R:Schmelzer, H.

Adv. Gene Technol. 21, 228-229, 1984

A&gt;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.

A:Reference number: I51851

A:Accession: I51851

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA



A:Reference number: I58390; MUID:93205410; PMID:8455946  
A:Accession: A158390  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1257 <OTT1>  
A:Cross-references: GB:S57153; NID:9298681; PIDN:AAB25833.1; PID:9298682  
A:Accession: I78883  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 338-384, 'V', 386-617, 'R', 619-652, 'V', 654-778, 'T', 780-1120, 1175-1257 <OTT2>  
A:Cross-references: GB:S57160; NID:9298683; PIDN:AAB25834.1; PID:9298684  
R:DeGee-Jones, D.; Huang, P.S.; Jones, R.E.; Haskell, K.M.; Vuocolo, G.A.; Hanobik, M.G.  
Nature 352, 251-254, 1991  
A:Title: Cloning of cDNAs for cellular proteins that bind to the retinoblastoma gene product  
A:Reference number: S16953; MUID:91312450; PMID:1857421  
A:Accession: S16953  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 855-1177, 'S', 1179-1195, 'SENIICL' <DEP>  
R:Kaelin Jr., W.G.; Krek, W.; Sellers, W.R.; DeCaprio, J.A.; Ajchenbaum, F.; Fuchs, C.S.  
Cell 70, 351-364, 1992  
A:Title: Expression cloning of a cDNA encoding a retinoblastoma-binding protein with E2F  
A:Reference number: A42997; MUID:92346721; PMID:1638635  
A:Accession: A42997  
A:Molecule type: mRNA  
A:Residues: 'MTMKL', 510-617, 'R', 619-1257 <KA5>  
A:Experimental source: Akata cells  
A:Note: the cited GenBank accession number, M96577, is apparently a misprint and does not  
A:Note: sequence extracted from NCBI backbone (NCBIN:110020, NCBI:110022)  
C:Genetics:  
A:Gene: GDB:RBPI  
A:Cross-references: GDB:120340; OMIM:180260  
A:Map position: 3q21-3q22  
C:Superfamily: human retinoblastoma binding protein 1  
C:Keywords: alternative splicing  
F:1-1257/Product: retinoblastoma binding protein 1, splice form I #status predicted <SF1  
F:1-1120,1175-1257/Product: retinoblastoma binding protein 1, splice form II #status pre  
Query Match 37.6%; Score 62; DB 1; Length 1257;  
Best Local Similarity 40.0%; Pred. No. 25;  
Matches 10; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
QY 9 NXGKHLNKSXERVWLRKQLQDVHNY 33  
|: ::||::|:|:|:|:|:  
DB 1175 NELDNMNSTERISFLQKLEIRKY 1199  
RESULT 10  
BBHU  
complement factor B precursor [validated] - human  
N:Alternate names: C3 convertase; C3 proactivator; glycine-rich beta-glycoprotein; heat-  
N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) Bb fragment  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1984 #sequence revision 05-Aug-1994 #text change 09-Jul-2004  
C:Accession: S34075; A44622; A00934; A19188; A19947; B25971; S14339; A44628; 154  
R:Mejia, J.E.; Jahn, I.; de la Salle, H.; Hauptmann, G.  
submitted to the EMBL Data Library, March 1993  
A:Reference number: S34075  
A:Accession: S34075  
A:Molecule type: mRNA  
A:Residues: 1-764 <MEU>  
A:Cross-references: UNIPROT:P00751; EMBL:X72875; NID:9237568; PIDN:CAAS1389.1; PID:g2975  
R:Woods, D.E.; Markham, A.F.; Ricker, A.T.; Goldberger, G.; Colten, H.R.  
Proc. Natl. Acad. Sci. U.S.A. 79, 5661-5665, 1982  
A:Title: Isolation of cDNA clones for the human complement protein factor B, a class III  
A:Reference number: A44622; MUID:83039428; PMID:6957884  
A:Accession: A44622  
A:Molecule type: mRNA  
A:Residues: 467-546; 550-595; 752-764 <WOO>  
A:Cross-references: GB:J00185; GB:J00186  
A:Note: the authors translated the codon TAC at 519 as Thr; the nucleic acid translation  
R:Moie, J.E.; Anderson, J.K.; Davison, E.A.; Woods, D.E.  
J. Biol. Chem. 259, 3407-3412, 1984  
A:Title: Complete primary structure for the zymogen of human complement factor B.  
A:Reference number: A20751; MUID:84161997; PMID:6546754  
A:Accession: A00934  
A:Molecule type: protein; mRNA  
A:Residues: 26-764 <MOI>  
A:Cross-references: GB:K01566  
A:Note: nucleic acid translation differs from the sequence shown in having 300-Leu, 328-V  
A:Note: 736-Ser was also found  
R:Christie, D.L.; Gagnon, J.  
Biochem. J. 209, 61-70, 1983  
A:Title: Amino acid sequence of the Bb fragment from complement factor B. Sequence of the  
A:Reference number: A19188; MUID:83204002; PMID:6342610  
A:Contents: the final paper in a series documenting the sequence, glycosylation site, and  
A:Accession: A19188  
A:Molecule type: protein  
A:Residues: 260-296, 'T', 298-764 <CHR>  
R:Campbell, R.D.; Porter, R.R.  
Proc. Natl. Acad. Sci. U.S.A. 80, 4464-4468, 1983  
A:Title: Molecular cloning and characterization of the gene coding for human complement f  
A:Reference number: A19947; MUID:83273641; PMID:6308626  
A:Accession: A19947  
A:Molecule type: DNA  
A:Residues: 346-764 <CAM>  
A:Cross-references: GB:J00125  
A:Accession: B19947  
A:Molecule type: mRNA  
A:Residues: 339-509 <CA1>  
A:Cross-references: GB:J00126; NID:9187723; PIDN:AAA36226.1; PID:9553536  
R:Wu, L.; Morley, B.J.; Campbell, R.D.  
Cell 48, 331-342, 1987  
A:Title: Cell-specific expression of the human complement protein factor B gene: evidence  
A:Reference number: A25971; MUID:87102880; PMID:3643061  
A:Accession: B25971  
A:Molecule type: DNA  
A:Residues: 1-99 <WUL>  
A:Cross-references: GB:M15082; NID:9187699; PIDN:AAA59625.1; PID:9553534  
R:Niemann, M.A.; Bhow, A.S.; Miller, E.J.  
Biochem. J. 274, 473-480, 1991  
A:Title: The principal site of glycation of human complement Factor B.  
A:Reference number: S14339; MUID:91174758; PMID:2006911  
A:Accession: S14339  
A:Molecule type: protein  
A:Residues: 270-329 <NIE>  
A:Note: binding site for carbohydrate to lysine under artificial conditions  
R:Morley, B.J.; Campbell, R.D.  
EMBO J. 3, 153-157, 1984  
A:Title: Internal homologies of the Ba fragment from human complement component factor B,  
A:Reference number: A44628; MUID:84158524; PMID:6323161  
A:Accession: A44628  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 16-225, 'F', 227-259 <MOR>  
R:Schwaebler, W.; Luttig, B.; Sokolowski, T.; Estaller, C.; Weiss, E.H.; Meyer zum Buscher  
Immunobiology 188, 221-232, 1993  
A:Title: Human complement factor B: functional properties of a recombinant zymogen of the  
A:Reference number: I54409; MUID:94041399; PMID:8225386  
A:Accession: I54409  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-764 <RES>  
A:Cross-references: GB:S67310; NID:9452937; PIDN:AAD13989.1; PID:g4261689  
R:Horuchi, T.; Kim, S.; Matsumoto, M.; Watanabe, I.; Fujita, S.; Volanakis, J.E.  
Mol. Immunol. 30, 1587-1592, 1993  
A:Title: Human complement factor B: cDNA cloning, nucleotide sequencing, phenotypic conve  
A:Reference number: I57824; MUID:94067177; PMID:8247029  
A:Accession: I57824  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-31, 'Q', 33-764 <RE2>  
A:Cross-references: GB:L15702; NID:9291921; PIDN:AAA16820.1; PID:g291922  
C:Comment: 292-Cys has a free sulfhydryl.  
C:Genetics:

A;Gene: GDB:BF  
A;Cross-references: GDB:119726; OMIM:138470  
A;Map position: 6p21.3-6p21.3  
A;Introns: 21/3; 99/3; 346/1; 390/1; 424/1; 470/1; 502/3; 542/1; 593/2; 619/1; 652/3; 69  
A;Note: The list of introns may be incomplete  
A;Note: gene is located in the major histocompatibility complex, class III region  
C;Complex: complement factor B initially forms an inactive complex with complement fact  
ment factor C3b forming active C3/C5 convertase; Ba is released  
C;Function:  
A;Description: Bb is a serine proteinase; C3/C5 convertase cleaves complement C3 alpha c  
al  
A;Pathway: complement alternate pathway  
C;Superfamily: complement B/C2; complement factor H repeat homology; trypsin homology; v  
C;Keywords: acute phase; complement alternate pathway; duplication; glycoprotein; hydro  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-764/Product: complement factor B #status experimental <WAT>  
F;26-259/Product: complement factor B fragment #status experimental <BAF>  
F;37-98/Domain: complement factor H repeat homology <FH1>  
F;103-158/Domain: complement factor H repeat homology <FH2>  
F;165-218/Domain: complement factor H repeat homology <FH3>  
F;260-764/Product: C3/C5 convertase Bb fragment #status experimental <BBF>  
F;268-458/Domain: von Willebrand factor type A repeat homology <VFA>  
F;482-752/Domain: trypsin homology #status atypical <TRY>  
F;37-76.62-98.103-145.131-158.165-205.191-218.478-596.511-527.599-615.656-682.695-725/D  
F;122.142.285.378/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F;258-260/Cleavage site: Arg-Lys (complement factor D) #status experimental  
F;526.576.699/Active site: His, Asp, Ser #status experimental  
Query Match 36.4%; Score 60; DB 1; Length 764;  
Best Local Similarity 34.6%; Pred. No. 26;  
Matches 9; Conservative 10; Mismatches 7; Indels 0; Gaps 0;  
QY 4 EIQHXGKHLNSXERVWLRKKLQD 29  
DB 733 QVPARDFHINLQVLPWLKRLQD 758  
RESULT 11  
T00065  
hypotheical protein KIAA0442 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 09-Jul-2004  
C;Accession: T00065  
R;Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.  
DNA Res. 4, 307-313, 1997  
A;Title: Prediction of the coding sequences of unidentified human genes. VIII. 78 new c  
A;Reference number: Z14084; MUID:98116655; PMID:9455477  
A;Accession: T00065  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-1172 <ISH>  
A;Cross-references: UNIPROT:Q8WXX7; EMBL:AB007902; NID:g2662164; PIDN:BAA23714.1; PID:g2  
C;Genetics:  
A;Note: KIAA0442  
Query Match 35.5%; Score 58.5; DB 2; Length 1172;  
Best Local Similarity 36.1%; Pred. No. 60;  
Matches 13; Conservative 8; Mismatches 10; Indels 5; Gaps 1;  
QY 1 SVSEIQHXGKHLNSXERVWLRK-----KLQDVH 31  
DB 1049 SVDPRHERGGHLDERHLMLREDYEHTRLSVH 1084  
RESULT 12  
A27605  
dystrophin, muscle - human  
N;Alternate names: Duchenne muscular dystrophy protein  
C;Species: Homo sapiens (man)  
C;Date: 19-Nov-1988 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
C;Accession: A27605; S07710; A27162; S05291; A40134; S06051; S10346; S02243; S02242; S02  
R;Koenig, M.; Monaco, A.P.; Kunkel, L.M.

Cell 53, 219-228, 1988  
A;Title: The complete sequence of dystrophin predicts a rod-shaped cytoskeletal protein.  
A;Reference number: A27605; MUID:88194521; PMID:3282674  
A;Accession: A27605  
A;Molecule type: mRNA  
A;Residues: 1-3685 <KOE>  
A;Cross-references: UNIPROT:Q14205; GB:M18533; NID:g181856; PIDN:AAA53189.1; PID:g181857  
R;Rosenthal, A.; Speer, A.; Billwiltz, H.; Cross, G.S.; Forrest, S.M.; Davies, K.E.  
Nucleic Acids Res. 17, 5391, 1989  
A;Title: Two human cDNA molecules coding for the Duchenne muscular dystrophy (DMD) locus  
A;Reference number: S07710; MUID:89345106; PMID:2668885  
A;Accession: S07710  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-132, 'P', 134-622, 'I', 624-783, 'G', 785-1196, 'F', 1198-1376, 'N', 1378-1468, 'Q', 14  
A;Cross-references: EMBL:X14298; NID:g30845; PIDN:CAA32479.1; PID:g30846  
A;Note: this sequence was submitted to the EMBL Data Library, February 1989  
R;Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.  
Cell 50, 509-517, 1987  
A;Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary s  
A;Reference number: A90897; MUID:87273512; PMID:3607877  
A;Accession: A27162  
A;Molecule type: mRNA  
A;Residues: 1-497 <KOE>  
A;Cross-references: GB:M18533  
R;Cross, G.S.; Speer, A.; Rosenthal, A.; Forrest, S.M.; Smith, T.J.; Edwards, Y.; Flint,  
EMBO J. 6, 3277-3283, 1987  
A;Title: Deletions of fetal and adult muscle cDNA in Duchenne and Becker muscular dystro  
A;Reference number: S01263; MUID:88111512; PMID:3428261  
A;Accession: S05291  
A;Molecule type: mRNA  
A;Residues: 404-556, 'T', 558-610, 'K', 612-622, 'I', 624-664, 'M', 665-783, 'G', 785-1137, 'PN' <C  
A;Cross-references: EMBL:X06178  
A;Note: 475-Ile and 529-Glu were also found  
R;Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.  
Science 238, 347-350, 1987  
A;Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.  
A;Reference number: A40134; MUID:88018015; PMID:3659917  
A;Accession: A40134  
A;Molecule type: mRNA  
A;Residues: 491-1207 <HOF>  
A;Cross-references: GB:M18533  
R;Blonden, L.A.J.; den Dunnen, J.T.; van Paassen, H.M.B.; Wapenaar, M.C.; Grootsholten,  
Nucleic Acids Res. 17, 5611-5621, 1989  
A;Title: High resolution deletion breakpoint mapping in the DMD gene by whole cosmid hybr  
A;Reference number: S06051; MUID:89345155; PMID:2569720  
A;Accession: S06051  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 2147-2204 <BLO>  
A;Cross-references: EMBL:X51934  
R;Speer, A.; Billwiltz, H.; Huth, A.; Coutelle, C.; England, S.; Love, D.; Davies, K.E.  
submitted to the EMBL Data Library, February 1990  
A;Reference number: S10346  
A;Accession: S10346  
A;Molecule type: DNA  
A;Residues: 2438-2480 <SPE>  
A;Cross-references: EMBL:X51934  
R;Chamberlain, J.S.; Gibbs, R.A.; Ranier, J.E.; Nguyen, P.N.; Caskey, C.T.  
Nucleic Acids Res. 16, 11141-11156, 1988  
A;Title: Deletion screening of the Duchenne muscular dystrophy locus via multiplex DNA an  
A;Reference number: S02109; MUID:89083552; PMID:3205741  
A;Accession: S02243  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 665-722 <CHA>  
A;Cross-references: EMBL:X13045; NID:g30825; PIDN:CAA31451.1; PID:g1335048  
A;Accession: S02242  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 2098-2146 <CH2>  
A;Cross-references: EMBL:X13046; NID:g30827; PIDN:CAA31452.1; PID:g809549  
A;Accession: S02244

A>Status: preliminary; translation not shown  
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A:Accession: S02109  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 2305-2365, 'K' <CH4>  
A:Cross-references: EMBL:X13047; NID:g30831; PIDN:CAA31453.1; PID:g1335050  
R:Ginjaar, I.H.B.; van Paassen, M.H.M.B.; den Dunnen, J.J.T.; van Ommen, G.G.J.B.  
submitted to the EMBL Data Library, March 1992  
A:Description: Sequence of Duchenne muscular dystrophy gene exon 60, located directly 5'  
A:Reference number: S23736  
A:Accession: S23736  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 2980-2995, 'K', 2997-3028 <GIN>  
R:Heilig, R.; Lemaire, C.; Mandel, J.L.  
Nucleic Acids Res. 15, 9129-9142, 1987  
A:Title: A 230kb cosmid walk in the Duchenne muscular dystrophy gene: detection of a con  
A:Reference number: S09071; MUID:88067745; PMID:2825128  
A:Accession: S09071  
A:Molecule type: DNA  
A:Residues: 'SGGHSWTIHCSLYRLPLTLI', 218-277 <HEI>  
A:Cross-references: EMBL:X06293; EMBL:Y00494  
A:Note: sequence N-terminal of residue 218 correspond to a putative exon  
R:Roberts, R.G.; Coffey, A.J.; Bobrow, M.; Bentley, D.R.  
Genomics 16, 536-538, 1993  
A:Title: Exon structure of the human dystrophin gene.  
A:Reference number: I54186; MUID:93300536; PMID:8314593  
A:Accession: I54186  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A:Molecule type: DNA  
A:Residues: 984-1411 <RE3>  
A:Cross-references: GB:L05642; NID:g181892; PIDN:AAA74506.1; PID:g950344  
A:Accession: I68509  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A:Molecule type: DNA  
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A:Cross-references: GB:L05646; NID:g181896; PIDN:AAA74507.1; PID:g950345  
A:Accession: I68510  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A:Molecule type: DNA  
A:Residues: 2850-2979 <ROB>  
A:Cross-references: GB:L05649; NID:g181899; PIDN:AAA74508.1; PID:g950346  
R:Roberts, R.G.; Coffey, A.J.; Bobrow, M.; Bentley, D.R.  
Genomics 13, 942-950, 1992  
A:Title: Determination of the exon structure of the distal portion of the dystrophin gen  
A:Reference number: I54175; MUID:92372062; PMID:1505985  
A:Accession: I54175  
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL  
A:Molecule type: DNA  
A:Residues: 2980-3685 <RES>  
A:Cross-references: GB:M86903; NID:g181881; PIDN:AAA35779.1; PID:g457519  
R:Enrenpreis, J.; Hilliers, M.; Junkes, B.; Pfordt, M.; Schwinger, E.; Vosberg, H.P.  
Genomics 10, 551-557, 1991  
A:Title: Analysis of a dystrophin gene deletion by amplification of mRNA isolated from D  
A:Reference number: I54166; MUID:91365360; PMID:1889805  
A:Accession: I54166  
A>Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 2250-2254 <RE4>  
A:Cross-references: GB:S54699; NID:g235303; PIDN:AAB19754.1; PID:g235304  
R:Feener, C.A.; Koenig, M.; Kunkel, L.M.  
Nature 338, 509-511, 1989  
A:Title: Alternative splicing of human dystrophin mRNA generates isoforms at the carboxy  
A:Reference number: S03902; MUID:89181947; PMID:2648158  
A:Accession: S03902  
A:Molecule type: mRNA  
A:Residues: 'MED', 12-32; 3377-3408 <FEE>  
A:Cross-references: EMBL:X15148  
C:Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the pl

C:Comment: Defects in dystrophin are responsible for the Duchenne/Becker muscular dystrophy

C:Genetics: A:Gene: GDB:DMD

A:Cross-references: GDB:119850; OMIM:310200

A:Map position: Xp21.2-Xp21.2

A:Introns: 11/1; 31/3; 62/3; 88/3; 119/3; 177/2; 217/1; 277/3; 320/3; 383/3; 444/2; 494/3

3: 3055/1; 3075/2; 3096/1; 3121/1; 3188/2; 3217/1; 3269/3; 3325/2; 3362/3; 3408/2; 3421/2

A:Note: the list of introns is incomplete

C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin

C:Keywords: actin binding; alternative splicing; calmodulin binding; cytoskeleton; leucine elix

F:14-233/Domain: alpha-actinin actin-binding domain homology <ACT>

F:253-327/Region: hinge

F:338-447/Domain: spectrin/dystrophin repeat homology <SP01>

F:448-556/Domain: spectrin/dystrophin repeat homology <SP02>

F:558-667/Domain: spectrin/dystrophin repeat homology <SP03>

F:668-717/Region: hinge

F:718-828/Domain: spectrin/dystrophin repeat homology <SP04>

F:836-934/Domain: spectrin/dystrophin repeat homology <SP05>

F:938-1045/Domain: spectrin/dystrophin repeat homology <SP06>

F:1047-1154/Domain: spectrin/dystrophin repeat homology <SP07>

F:1156-1263/Domain: spectrin/dystrophin repeat homology <SP08>

F:1365-1367/Domain: spectrin/dystrophin repeat homology <SP09>

F:1372-1477/Domain: spectrin/dystrophin repeat homology <SP10>

F:1478-1568/Domain: spectrin/dystrophin repeat homology #status atypical <SP11>

F:1570-1676/Domain: spectrin/dystrophin repeat homology <SP12>

F:1678-1782/Domain: spectrin/dystrophin repeat homology <SP13>

F:1784-1875/Domain: spectrin/dystrophin repeat homology #status atypical <SP14>

F:1876-1982/Domain: spectrin/dystrophin repeat homology <SP15>

F:1984-2101/Domain: spectrin/dystrophin repeat homology <SP16>

F:2103-2208/Domain: spectrin/dystrophin repeat homology <SP17>

F:2210-2316/Domain: spectrin/dystrophin repeat homology <SP18>

F:2327-2423/Domain: spectrin/dystrophin repeat homology <SP19>

F:2424-2470/Region: hinge

F:2471-2577/Domain: spectrin/dystrophin repeat homology <SP20>

F:2579-2686/Domain: spectrin/dystrophin repeat homology <SP21>

F:2688-2802/Domain: spectrin/dystrophin repeat homology <SP22>

F:2804-2931/Domain: spectrin/dystrophin repeat homology <SP23>

F:2933-3040/Domain: spectrin/dystrophin repeat homology <SP24>

F:3041-3112/Region: hinge

F:3055-3092/Domain: WW repeat homology <WW1>

F:3080-3360/Region: cysteine-rich

F:3506-3527/Region: leucine zipper motif

F:3572-3593/Region: leucine zipper motif

Query Match 35.2%; Score 58; DB 1; Length 3685;

Best Local Similarity 37.5%; Pred. No. 2.2e+02;

Matches 12; Conservative 10; Mismatches 8; Indels 2; Gaps 1;

Qy 1 SVSIIQHNKKHL--NSXREVEWLKKLDV 30

Db 1423 SLEEMKHNQKEAAQRVLSDIVAAKKLDV 1454

RESULT 13

T44470

C:Species: Shigella flexneri

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C:Accession: T44470

R:Moss, J.E.; Cardozo, T.J.; Zychlinsky, A.; Groisman, E.A.

Mol. Microbiol. 33, 74-83, 1999

A:Title: The selC-associated SH-2 pathogenicity island of Shigella flexneri.

A:Reference number: 2227779; MUID:99340540; PMID:10411725

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-118 <MOS>

A:Cross-references: UNIPROT:Q9XC10; EMBL:AF141323; NID:g5532445; PIDN:AAD44737.1; PID:g55

A:Experimental source: strain M90T; serotype 5a

C:Genetics: A:Gene: tnpD







DE Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).  
GN Name=PTH;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A. PubMed=6950381;  
RX MEDLINE=82150870; PubMed=6950381;  
RA Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;  
RT "Nucleotide sequence of cloned cDNAs encoding human preproparathyroid  
RT hormone";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=83169834; PubMed=6220408;  
RA Vasicek T.J., McDevitt B.E., Freeman M.W., Fennick B.J., Hendy G.N.,  
RA Potts J.T. Jr., Rich A., Kronenberg H.M.;  
RT "Nucleotide sequence of the human parathyroid hormone gene";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).  
RN [3]  
RN SEQUENCE OF 26-37. PubMed=4833516;  
RX MEDLINE=74174967; PubMed=4833516;  
RA Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;  
RT "Structural analysis of human parathyroid hormone by a new  
RT microsequencing approach";  
RL Nature 249:155-157(1974).  
RN [4]  
RN SEQUENCE OF 26-40.  
RX MEDLINE=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).  
RN [5]  
RN SEQUENCE OF 32-68.  
RX MEDLINE=74111656; PubMed=4521809;  
RA Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,  
RA O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;  
RT "The amino-acid sequence of the amino-terminal 37 residues of human  
RT parathyroid hormone";  
RL Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).  
RN [6]  
RN SEQUENCE OF 61-83 AND 84-115.  
RX MEDLINE=79082855; PubMed=728431;  
RA Keutmann H.T., Sauer M.W., Hendy G.N., O'Riordan J.L.H.,  
RA Potts J.T. Jr.;  
RT "Complete amino acid sequence of human parathyroid hormone";  
RL Biochemistry 17:5723-5729(1978).  
RN [7]  
RN SEQUENCE OF 75-100.  
RX MEDLINE=75146516; PubMed=1125201;  
RA Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,  
RA O'Riordan J.L.H., Potts J.T. Jr.;  
RL (In) Talmadge R.V., Owen M., Parsons J.A. (eds.);  
RL Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,  
RL Amsterdam (1975).  
RN [8]  
RN REVISIONS.  
RX MEDLINE=75146516; PubMed=1125201;  
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "A reinvestigation of the amino-terminal sequence of human parathyroid  
RT hormone";  
RL Biochemistry 14:1842-1847(1975).  
RN [9]  
RN SYNTHESIS OF 32-65.  
RX MEDLINE=75059220; PubMed=4474131;  
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T.,  
RA Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;  
RT "Solid-phase synthesis of the biologically active N-terminal 1-34  
RT peptide of human parathyroid hormone";  
RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).  
RN [10]  
RN SYNTHESIS OF 32-65.  
RX MEDLINE=73227467; PubMed=4721748;  
RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,  
RA Riniker B., Rittel W., Sieber P.;  
RT "Synthesis of sequence 1-34 of human parathyroid hormone";  
RL Helv. Chim. Acta 56:470-473(1973).  
RN [11]  
RN STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=91299748; PubMed=2069952;  
RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;  
RT "Investigation of the solution structure of the human parathyroid  
RT hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and  
RT molecular dynamics calculations";  
RL Biochemistry 30:6936-6942(1991).  
RN [12]  
RN STRUCTURE BY NMR OF 32-65.  
RX MEDLINE=93345518; PubMed=8344299;  
RA Barden J.A., Cuthbertson R.M.;  
RT "Stabilized NMR structure of human parathyroid hormone (1-34)";  
RL Eur. J. Biochem. 215:315-321(1993).  
RN [13]  
RN STRUCTURE BY NMR OF 32-68.  
RX MEDLINE=95318084; PubMed=7797503; DOI=10.1074/jbc.270.25.15194;  
RA Marx U.C., Austermann S., Bayer P., Forssmann W.-G., Rosch F.;  
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,  
RA Roesch P.;  
RT "Structure of human parathyroid hormone 1-37 in solution";  
RL J. Biol. Chem. 270:15194-15202(1995).  
RN [14]  
RN STRUCTURE BY NMR OF 32-70.  
RX MEDLINE=20090619; PubMed=10623601; DOI=10.1006/bbrc.1999.1958;  
RA Marx U.C., Austermann K., Bayer P., Forssmann W.-G., Rosch F.;  
RT "Solution structures of human parathyroid hormone fragments hPTH(1-34)  
RT and hPTH(1-39) and bovine parathyroid hormone fragment bPTH(1-37)";  
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).  
RN [15]  
RN VARIANT FTH ARG-18.  
RX MEDLINE=91009811; PubMed=2212001;  
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,  
RA Kronenberg H.M.;  
RT "Mutation of the signal peptide-encoding region of the  
RT preproparathyroid hormone gene in familial isolated  
RT hypoparathyroidism";  
RL J. Clin. Invest. 86:1084-1087(1990).  
RN [16]  
RN VARIANT FTH PRO-23.  
RX MEDLINE=91009811; PubMed=2212001;  
RA Sunthornchepvarakul T., Churesigaw S., Ngowngarmratana S.;  
RT "A novel mutation of the signal peptide of the preproparathyroid  
RT hormone gene associated with autosomal recessive familial isolated  
RT hypoparathyroidism";  
RL J. Clin. Endocrinol. Metab. 84:3792-3796(1999).  
RN [17]  
RN FUNCTION: PTH elevates calcium level by dissolving the salts in  
RN bone and preventing their renal excretion.  
RN [18]  
RN SUBCELLULAR LOCATION: Secreted.  
RN [19]  
RN DISEASE: Defects in PTH are a cause of familial isolated  
RN hypoparathyroidism (FIH) [MIM:146200]. FIH exist both as autosomal  
RN dominant and recessive forms of hypoparathyroidism.  
RN [20]  
RN SIMILARITY: Belongs to the parathyroid hormone family.  
RN [21]  
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RN [22]  
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RN EMBL; V00597; CAA23843.1; -;  
RN EMBL; A29146; CAA01956.1; -;  
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RN PDB; 1ET2; Model; A=32-65.

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DR PDB; 1HTH; NMR; @=32-65.
DR PDB; 1ZWA; NMR; @=32-65.
DR PDB; 1ZWB; NMR; @=33-68.
DR PDB; 1ZWD; NMR; @=34-68.
DR PDB; 1ZWE; NMR; @=35-68.
DR PDB; 1ZWF; NMR; @=34-68.
DR PDB; 1ZWG; NMR; @=34-68.
DR PDB; 1ZWG; NMR; @=34-68.
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DR MIM; 148200; -.
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DR GO; GO:0046058; P.cAMP metabolism; TAS.
DR GO; GO:0007267; P.cell-cell signaling; TAS.
DR GO; GO:0007186; P.G-protein coupled receptor protein signalin...; TAS.
DR GO; GO:0008628; P.induction of apoptosis by hormones; TAS.
DR GO; GO:0001501; P.skeletal development; TAS.
DR InterPro; IPR001415; Parathyroid hrm.
DR InterPro; IPR003625; Pthyrohm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR 3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW SIGNAL.
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FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT VARIAT 23 23
FT VARIAT 23 23
FT CONFLICT 107 107
FT HELIX 34 64
FT SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;
Query Match 91.2%; Score 150.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLQDVHNY 33
DB 32 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 65
RESULT 3
PTHY MACFA
ID PTHY MACFA STANDARD; PRT; 115 AA.
AC Q9XT35;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Malaivijitnond S., Takenaka O.;
RT "Nucleotide sequences of parathyroid gene in five species of macaque of Thailand."
RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PDB; 1ZWE; NMR; @=35-68.
DR PDB; 1ZWF; NMR; @=34-68.
DR PDB; 1ZWG; NMR; @=34-68.
DR PDB; 1ZWG; NMR; @=34-68.
DR MIM; 168450; -.
DR MIM; 148200; -.
DR GO; GO:0003179; F.hormone activity; TAS.
DR GO; GO:0046058; P.cAMP metabolism; TAS.
DR GO; GO:0007267; P.cell-cell signaling; TAS.
DR GO; GO:0007186; P.G-protein coupled receptor protein signalin...; TAS.
DR GO; GO:0008628; P.induction of apoptosis by hormones; TAS.
DR GO; GO:0001501; P.skeletal development; TAS.
DR InterPro; IPR001415; Parathyroid hrm.
DR InterPro; IPR003625; Pthyrohm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR 3D-structure; Direct protein sequencing; Disease mutation; Hormone;
KW SIGNAL.
FT SIGNAL. 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT VARIAT 23 23
FT VARIAT 23 23
FT CONFLICT 107 107
FT HELIX 34 64
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Query Match 91.2%; Score 150.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLQDVHNY 33
DB 32 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 65
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ID PTHY CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., Dewille J.W.,
RA Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone."
RL Gene 160:241-243(1995).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
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CC
DR EMBL; AF130257; AAD42777.1; -.
DR HSSP; P01270; 1ET1.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrohm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL. 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;
Query Match 91.2%; Score 150.5; DB 1; Length 115;
Best Local Similarity 85.3%; Pred. No. 1.2e-10;
Matches 29; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 SVSEIQ-XHNXGKHLNSXRVWLKRLQDVHNY 33
DB 32 SVSEIQLMHNLGKHLNSMERVWLKRLQDVHNF 65

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```
DR InterPro; IPR003625; Pthyrohm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25 By similarity.
FT PROPEP 26 31 By similarity.
FT CHAIN 32 115 Parathyroid hormone.
SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 88.2%; Score 145.5; DB 1; Length 115;
Best Local Similarity 82.4%; Pred. No. 4.8e-10;
Matches 28; Conservative 5; Mismatches 0; Indels 1; Gaps 1;

OY 1 SVSEIQ-XHNKGKHLNSKXRVWLKRLKQDVHNY 33
   ||||| :|||:|||||:|||||:|||||:
Db 32 SVSEIQFMHNLGKHLSSMERVWLKRLKQDVHNF 65

RESULT 5
PTHY_PIG ID PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
[2]
RN SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine parathyroid hormone. Identification, biosynthesis, and
RT partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
[3]
RN SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
RA Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
CC bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
-----
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-----
DR EMBL; X05722; CAA29193.1; -.
DR F01; B26806; PTPG.
DR HSSP; P01270; 1BWV.
DR InterPro; IPR001415; Parathyroid_hrm.
DR InterPro; IPR003625; Pthyrohm_sub.
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DR Pfam; PF01279; Parathyroid; 1.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD010687; Pthyrohm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Direct protein sequencing; Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 Parathyroid hormone.
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 88.2%; Score 145.5; DB 1; Length 115;
Best Local Similarity 82.4%; Pred. No. 4.8e-10;
Matches 28; Conservative 5; Mismatches 0; Indels 1; Gaps 1;

OY 1 SVSEIQ-XHNKGKHLNSKXRVWLKRLKQDVHNY 33
   ||||| :|||:|||||:|||||:|||||:
Db 32 SVSEIQFMHNLGKHLSSMERVWLKRLKQDVHNF 65

RESULT 6
PTHY_BOVIN ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN Name=PTH;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDewitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
RA Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RT preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RT at the 5' terminus of the sense strand of bovine parathyroid hormone
RT cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=83105964; PubMed=6185374; DOI=10.1016/0303-7207(82)90136-8;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=84262483; PubMed=6086460; DOI=10.1016/0378-1119(84)90149-5;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RT parathyroid hormone.";
RL Gene 28:319-329(1984).
[5]
RN SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine preproparathyroid
RT hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
[6]
RN SEQUENCE OF 32-115.
```





```
DR PROSITE; PS00335; PARATHYROID; 1.
KW Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 32 115 parathyroid hormone.
SQ SEQUENCE 115 AA; 12825 MW; DA3FABBCB4E2FD9 CRC64;

Query Match
Best Local Similarity 77.3%; Score 127.5; DB 2; Length 115;
Matches 23; Conservative 9; Mismatches 1; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLRKKLQDVHNY 33
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
32 AVSEIQLMHNLGKHLASMERMQWLRRKLQDMENP 65

RESULT 11
PTHY_CHICK
ID PTHY_CHICK STANDARD; PRT; 119 AA.
AC P15743;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone precursor (PTH).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89219100; PubMed=2710135;
RA Russell J., Sherwood L.M.;
RT "Nucleotide sequence of the DNA complementary to avian (chicken)
preparathyroid hormone mRNA and the deduced sequence of the hormone
precursor.";
RL Mol. Endocrinol. 3:325-331 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89284968; PubMed=3251402;
RA Khosla S., Denay M., Pines M., Hurwitz S., Potts J.T. Jr.,
Kronenberg H.M.;
RT "Nucleotide sequence of cloned cDNAs encoding chicken
preparathyroid hormone.";
RL J. Bone Miner. Res. 3:689-698 (1988).
CC -!- FUNCTION: PTH elevates calcium level by dissolving the salts in
bone and preventing their renal excretion.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the parathyroid hormone family.
-----
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-----
DR EMBL; M31604; AAA49093.1; -.
DR EMBL; M36522; AAB02866.1; -.
DR PIR; A34937; A34937.
DR HSP; P01270; 1FVY.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR PIRSF; PIRSF001832; PTH; 1.
DR ProDom; PD013225; PTH related; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 119 Parathyroid hormone.
```

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SQ SEQUENCE 119 AA; 13943 MW; B309D8E772997F6E CRC64;

Query Match
Best Local Similarity 62.1%; Score 102.5; DB 1; Length 119;
Matches 19; Conservative 10; Mismatches 3; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLRKKLQDVHNY 32
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:
32 SVSEQLMHNLEHRRHTVERQDLQWLQMKLQDVHS 64

RESULT 12
QW9J4
ID QW9J4 PRELIMINARY; PRT; 91 AA.
AC Q6W9J4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Parathyroid hormone type-2.
GN Name=PTH;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14684608; DOI=10.1210/en.2003-0964;
RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,
Bastepe M., Rubin D.A., Juppner H.;
RT "Identification and characterization of two parathyroid hormone-like
molecules in zebrafish.";
RL Endocrinology 145:1634-1639 (2004).
DR EMBL; AY302221; AAQ73561.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007595; P:lactation; IEA.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR InterPro; IPR003626; PTH related.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR ProDom; PD013225; PTH related; 2.
DR SMART; SM00087; PTH; 1.
SQ SEQUENCE 91 AA; 10647 MW; 75BBA25CEA64BF68 CRC64;

Query Match
Best Local Similarity 47.0%; Score 77.5; DB 2; Length 91;
Matches 14; Conservative 11; Mismatches 5; Indels 1; Gaps 1;

QY 1 SVSEIQ-XHNKGKHLNSXRVWLRKKLQDV 30
Db :||||:||||:||||:||||:||||:||||:||||:||||:
30 TISEQLMHNVRHKKQVGERQDLQWLQEKLDV 60

RESULT 13
QWQ25
ID QWQ25 PRELIMINARY; PRT; 102 AA.
AC Q6WQ25;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Parathyroid hormone ligand type-1.
GN Name=pth1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14684608; DOI=10.1210/en.2003-0964;
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RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,  
RA Bastepe M., Rubin D.A., Juppner H.;  
RT "Identification and characterization of two parathyroid hormone-like  
RT molecules in zebrafish.";  
RL Endocrinology 145:1634-1639(2004).  
DR EMBL; AY275669; AAQ16566.1; -.  
DR ZFIN; ZDB-GENE-040623-1; pth1.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR001415; P:thyroid hrm.  
DR InterPro; IPR003625; P:thyroid hrm.  
DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD010687; P:thyroid\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
SQ SEQUENCE 102 AA; 11690 MW; 5AA7A84FFA110764 CRC64;

Query Match 43.3%; Score 71.5; DB 2; Length 102;  
Best Local Similarity 40.6%; Pred. No. 0.54;  
Matches 13; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGKHLNSXERVELRKKLQDVH 31  
Db 36 AVNEVQLMHNIGVHKHVELRQDLQMKLGRGH 67

## RESULT 14

Q6WQ24 PRELIMINARY; PRT; 99 AA.  
ID Q6WQ24;  
AC Q6WQ24;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Parathyroid hormone ligand type-2.  
GN Name=pth2;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]

RP SEQUENCE FROM N.A.  
RX PubMed=14684608; DOI=10.1210/en.2003-0964;  
RA Gensure R.C., Ponugoti B., Gunes Y., Papasani M.R., Lanske B.,  
RA Bastepe M., Rubin D.A., Juppner H.;  
RT "Identification and characterization of two parathyroid hormone-like  
RT molecules in zebrafish.";  
RL Endocrinology 145:1634-1639(2004).  
DR EMBL; AY275670; AAQ16567.1; -.  
DR ZFIN; ZDB-GENE-040623-2; pth2.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR001415; P:thyroid hrm.  
DR InterPro; IPR003625; P:thyroid hrm.  
DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD010687; P:thyroid\_sub; 1.  
DR SMART; SM00087; PTH; 1.  
SQ SEQUENCE 99 AA; 11569 MW; 7F8BF84A7CA4D62 CRC64;

Query Match 41.5%; Score 68.5; DB 2; Length 99;  
Best Local Similarity 38.7%; Pred. No. 1.2;  
Matches 12; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Qy 1 SVSEIQ-XHNKXGKHLNSXERVELRKKLQDV 30  
Db 34 SISEVQLMHNVRHEKMLDRLQDLQLKLNNI 64

## RESULT 15

Q918E9 PRELIMINARY; PRT; 163 AA.  
ID Q918E9  
AC Q918E9;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Parathyroid hormone-related protein precursor.  
GN Name=PHR2;  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20314478; PubMed=10854780; DOI=10.1016/S0378-1119(00)00167-0;  
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,  
RA Elgar G., Clark M.S.;  
RT "Genomic structure and expression of parathyroid hormone-related  
RT protein in a teleost, Fugu rubripes.";  
RL Gene 250:67-76(2000).  
DR EMBL; AJ249391; CAB94712.1; -.  
DR HSSP; P12272; 1BZG.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR GO; GO:0007595; P:lactation; IEA.  
DR InterPro; IPR001415; Parathyrd hrm.  
DR InterPro; IPR003626; PTH related.  
DR Pfam; PF01279; Parathyroid; 1.  
DR ProDom; PD013225; PTH\_related; 1.  
KW Signal.  
FT SIGNAL 1 34 Potential.  
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;  
Query Match 40.3%; Score 66.5; DB 2; Length 163;  
Best Local Similarity 43.8%; Pred. No. 3.7; Mismatches 10; Indels 1; Gaps 1;  
Matches 14; Conservative 7;

Qy 1 SVSEIQ-XHNKXGKHLNSXERVELRKKLQDVH 31  
Db 38 SVSHAQLMHDKGRSLQBFRRRMWHLKLEEVH 69

Search completed: April 2, 2005, 00:11:45  
Job time : 182 secs